

APS/Bios
3/30/92

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(FILE 'USPAT' ENTERED AT 14:52:45 ON 30 MAR 92)

L1 161 S PDGF OR PLATELET DERIVED GROWTH FACTOR
L2 2545 S ENDOTHEL? OR FIBROBLAST
L3 106 S L1 AND L2
L4 1 S L3 AND 349
L5 2 S (36 OR 37 OR 38)(2W)(KD OR KILODALTON?) AND L3
L6 57 S (36 OR 37 OR 38)(2W)(KD OR KILODALTON?)
L7 67 S (36,000 OR 37,000 OR 38,000)(W)(MR OR MOLECULAR(W)WEIGHT
OR
L8 60 S L7 NOT L6
L9 117 S L6 OR L8
L10 3 S L9 AND L1

=> d ti ab in pddfd ccis 1-3

US PAT NO: 5,051,364 [IMAGE AVAILABLE] L10: 1 of 3
TITLE: Anti-lipocortin-I and anti-lipocortin-II monoclonal
 antibodies

ABSTRACT:

The present invention provides monoclonal antibodies which are specific for one but not both of human lipocortin-I and human lipocortin-II, as well as cultures of hybridomas and other types of cells producing such antibodies.

INVENTOR: Clare M. Isacke, La Jolla, CA
 Ian S. Trowbridge, San Diego, CA
 Tony Hunter, San Diego, CA

DATE ISSUED: Sep. 24, 1991

DATE FILED: Dec. 20, 1989

US-CL-CURRENT: 435/240.27; 424/85.8, 85.91; 435/70.21; 530/387, 389

US PAT NO: 4,935,233 [IMAGE AVAILABLE] L10: 2 of 3
TITLE: Covalently linked polypeptide cell modulators

ABSTRACT:

Described is a new class of polypeptide cell modulators characterized by being composed of two covalently linked cell modulators in a linear polypeptide sequence. Such dual function polypeptides have new and particularly useful activities when the component polypeptide cell modulators are interferons, lymphokines or cytotoxins which act through different and specific cell receptors to initiate complementary biological activities.

INVENTOR: Leslie D. Bell, Thame, United Kingdom
 Keith G. McCullagh, Princes Risborough, United Kingdom
 Alan G. Porter, High Wycombe, United Kingdom

DATE ISSUED: Jun. 19, 1990

DATE FILED: Dec. 2, 1985

US-CL-CURRENT: 424/85.5, 85.6, 85.7; 435/69.51; 530/351

US PAT NO: 4,543,439 L10: 3 of 3
TITLE: Production and use of monoclonal antibodies to
 phosphotyrosine-containing proteins

ABSTRACT:

A hybridoma cell line is disclosed that secretes monoclonal antibodies

which serve as a high titer, reproducible, biological reagent useful in biological/medical research for isolating and identifying phosphotyrosine-containing proteins. In addition, the antibodies have potential uses in diagnosis of a variety of diseases, including certain cancers. The antibodies, which have demonstrated affinity for a variety of molecules containing α -phosphotyrosine residues, were prepared using a synthetic analog, piazobenzyl phosphonate (ABP) covalently linked to a carrier protein, as the antigen.

INVENTOR: A. Raymond Frackelton, Jr., East Providence, RI
Herman N. Eisen, Waban, MA
Alonzo H. Ross, Bensalem, PA

DATE ISSUED: Sep. 24, 1985

DATE FILED: Dec. 13, 1982

US-CL-CURRENT: 435/70.21, 240.27, 948; 935/92

=>

2/7/1

9928438 BIOSIS Number: 93013438

DIFFERENTIAL BINDING BIOLOGICAL AND BIOCHEMICAL ACTIONS OF RECOMBINANT PDGF AA AB AND BB MOLECULES ON CONNECTIVE TISSUE CELLS

GROTENDORST G R; IGARASHI A; LARSON R; SOMA Y; CHARETTE M

DEP. CELL BIOLOGY ANATOMY, UNIV. MIAMI SCH. MED., P.O. BOX 016960, MIAMI, FLORIDA 33161.

J CELL PHYSIOL 149 (2). 1991. 235-243. CODEN: JCILLA

Full Journal Title: Journal of Cellular Physiology

Language: ENGLISH

We have compared the biological and biochemical properties of recombinant PDGF AA, AB, and BB using three types of fibroblastic cells: NIH/3T3, human skin fibroblast, and fetal bovine aortic smooth muscle. PDGF binding, receptor autophosphorylation, phosphatidyl inositol hydrolysis, as well as chemotactic and mitogenic responses of the cells were analyzed. PDGF-AB and PDGF-BB showed similar receptor binding, receptor autophosphorylation, and potent biological activity for all three of the cell types tested. In contrast, PDGF-AA was biologically active only for the NIH/3T3 cells in which binding sites for PDGF-AA were abundant, but was inactive for bovine aortic smooth muscle cells and human skin fibroblasts in which binding sites for PDGF-AA were absent. PDGF-AA could not induce any biochemical changes in the human skin fibroblasts or smooth muscle cells. Western blot studies with anti-Type .alpha. and .beta. PDGF receptor antibodies indicate that the NIH/3T3 cells contained both PDGF .alpha. and .beta. receptors, whereas the human skin fibroblasts and bovine smooth muscle cells contained only detectable levels of .beta. receptors. These results indicate that cells possessing high levels of PDGF .beta. receptors only are capable of responding equally well to either PDGF AB or BB.

2/7/2

6951686 BIOSIS Number: 87012287

KIDNEY EPITHELIAL CELLS EXPRESS C-SIS PROTOONCOGENE AND SECRET PDGF-LIKE PROTEIN

KARTHA S; BRADHAM D M; GROTENDORST G R; TOBACK F G

DEP. MED., BOX 453, UNIV. CHICAGO, 5841 SOUTH MARYLAND AVE., CHICAGO, ILL. 60637.

AM J PHYSIOL 255 (4 PART 2). 1988. F600-F606. CODEN: AJPHQ

Full Journal Title: American Journal of Physiology

Language: ENGLISH

Nontransformed monkey kidney cells (BSC-1 line), used as a model for renal epithelium, were assayed for release of platelet-derived growth factor (PDGF)-like proteins. BSC-1 cells continuously released a mitogenic activity for fibroblasts and a chemoattractant activity for smooth muscle cells, each of which was inhibited 80-90% by an antibody to human PDGF. A cDNA probe for the PDGF B-chain gene (c-sis), but not for the A-chain gene, hybridized to mRNA obtained from growing and quiescent cells. c-sis gene expression and PDGF-like protein secretion were studied in the presence of known growth-regulatory molecules. A secreted BSC-1 cell protein identical

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to transforming growth factor- β . β inhibited DNA synthesis in growing cultures and induced marked accumulation of c-sis mRNA without a corresponding increase in the release of PDGF-like activity. Adenosine diphosphate stimulated DNA synthesis in quiescent cultures and enhanced both c-cis expression and release of PDGF-like activity. However, growing the quiescent cells did not express the PDGF receptor gene or exhibit a mitogenic response to authentic PDGF. Thus the PDGF-like protein released by these kidney epithelial cells could contribute to growth control by a paracrine mechanism.

?s pdgf(w)like not s2

1829 PDGF
134382 LIKE
131 PDGF(W)LIKE
2 S2

S3 130 PDGF(W)LIKE NOT S2

?s s3 and (endothel? or fibroblast?)

130 S3
43997 ENDOTHEL?
65910 FIBROBLAST?

S4 61 S3 AND (ENDOTHEL? OR FIBROBLAST?)

?s s4 and ((36000(2n) molecular) or 36000(2w) (kd or kilodalton?) or (36000(2n) molecular) or ((36000(2n) (molecular or relative or dalton?))

>>>Command is too complex--please simplify

?s s4 and (349 or 36 or 36000)

61 S4
853 349
66080 36
78 36000
S5 2 S4 AND (349 OR 36 OR 36000)

?t s5/6/all

5/6/1

9100187 BIOSIS Number: 93085187

EFFECTS OF T CELLS ON PLATELET-DERIVED GROWTH FACTOR-LIKE PROTEIN SECRETION FROM ENDOTHELIAL CELLS

5/6/2

7179912 BIOSIS Number: 88102657

RETINAL PIGMENT EPITHELIAL CELLS PRODUCE PDGF-LIKE PROTEINS AND SECRETE THEM INTO THEIR MEDIA

?t s5/7/all

5/7/1

9100187 BIOSIS Number: 93085187

EFFECTS OF T CELLS ON PLATELET-DERIVED GROWTH FACTOR-LIKE PROTEIN SECRETION FROM ENDOTHELIAL CELLS

SHADDY R E; HANSEN J C; COWLEY C G
100 N. MEDICAL DRIVE, SALT LAKE CITY, UTAH 84113.
J HEART LUNG TRANSPLANT 11 (1 PART 1). 1992. 48-56. CODEN: JHLTE
Language: ENGLISH

The cause of accelerated graft arteriosclerosis after heart transplantation is unknown. To examine whether the interactions of T cells and endothelial cells (ECs) could contribute to the cause of this phenomenon, T cells were co-incubated with human umbilical artery endothelial cells (HUAEC) and human vein endothelial cells (HUEVC) and the resulting conditioned medium supernatant was assayed for the presence of platelet-derived growth factor (PDGF)-like protein. PDGF-like protein secretion was significantly greater from HUAECs co-incubated with T cells at T-cell/HUAEC ratios of 30:1 (6.9 \pm 1.1 fmol/106 ECs) and 10:1 (6.0 \pm 1.1 fmol/106 ECs) than the combined background secretion from HUAECs and T cells incubated separately (2.6 \pm 0.5 fmol/106 ECs).

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PDGF-like protein secretion above background levels from HUAECs was significantly greater, however, than from HUVECs co-incubated with T cells at T-cell/HUVEC ratios of 30:1 (1.8 +/- 0.4 fmol/10⁶ ECs) and 10:1 (0.75 fmol/10⁶ ECs) ($p < 0.05$). In four experiments, preincubation of HUAECs with gamma-interferon induced HLA-DR antigen expression but above background levels (3.0 +/- 0.6 fmol/10⁶ ECs) when compared to nonstimulated HUAECs (4.0 +/- 0.4 fmol/10⁶ ECs; $p < 0.05$). PDGF-like protein secretion was minimal at 1 hour and increased over time to a maximum at 24 hours. The conclusion is that T cells are capable of inducing secretion of a very potent mitogen, pdgf-like protein, from endothelial cells. This cell-inducing production of PDGF-like protein appears to be primarily or exclusively a property of arterial endothelial cells.

5/7/2

7179912 BIOSIS Number: 69102657

RETINAL PIGMENT EPITHELIAL CELLS PRODUCE PDGF-LIKE PROTEINS AND SECRETE THEM INTO THEIR MEDIA

CAMPOMCHIARO P A; SUGG R; GROTHENDORST G; HJELMELAND L M
DEP. OPHTHALMOL., UNIV. VA. SCH. MED., CHARLOTTESVILLE, VA. 22908.
EXP EYE RES 49 (2) 1989. 217-226. CODEN: EXERQ

Full Journal Title: Experimental Eye Research
Language: ENGLISH

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Human retinal pigment epithelial cells at confluence were used to condition serum-free Dulbecco's modified Eagle's medium. Conditioned media were exhaustively dialyzed against 0.5 N acetic acid, lyophilized, and subjected to Western blot analysis, using as primary antibody an IgG fraction prepared from goat antiserum directed against human platelet-derived growth factor. Native platelet-derived growth factor was resolved as a band with Mr of 38 kDa under non-reducing conditions, while bands with Mr of 36-38 kDa and 18.5 kDa were resolved from retinal pigment epithelial cell-conditioned media. Acid extracts of retinal pigment epithelial cells also contained bands at 36-38 kDa and media conditioned for 48 hr exhibited much denser bands than media conditioned for 24 hr. No bands were detected when non-immune goat IgG fractions were substituted for primary antibody and when conditioned media were prepared from several human fibroblast lines in the same manner as those prepared from retinal pigment epithelial cells, no detectable bands or only a faint shadow at 36 kDa were seen. Retinal pigment epithelial cell-conditioned media prepared in the presence of [³S]methionine were loaded on an anti-platelet-derived growth factor IgG affinity column, eluted, and subjected to SDS-polyacrylamide gel electrophoresis. Bands with Mr slightly less than 36 kDa and 18 kDa were visualized by autoradiography, demonstrating that the platelet-derived growth factor-like proteins in retinal pigment epithelial cell-conditioned media are newly synthesized. Two fractions eluted from the column also markedly stimulated fibroblast chemotaxis and incorporation of [³H]thymidine, both of which were neutralized by soluble anti-platelet-derived growth factor IgG. These data suggest that retinal pigment epithelial cells in culture produce platelet-derived growth factor-like proteins and secrete them into their media where they are capable of stimulating fibroblast chemotaxis and proliferation.

30mar92 15:25:56 User217743 Session D44.3

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\$3.00 6 Types

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\$1.25 DIALNET

\$14.69 Estimated cost this search

\$22.33 Estimated total session cost \$22.33 Mbytes
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IALNET: call cleared by request

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3. US-07-752-427-1 (1-2075)

HUMFGFAA Human fibroblast growth factor receptor mRNA, comp

LOCUS HUMFGFAA 3901 bp ss-mRNA PRI 15-MAR-1991
 DEFINITION Human fibroblast growth factor receptor mRNA, complete cds.
 ACCESSION M60485
 KEYWORDS
 SOURCE Human, cDNA to mRNA, clone f1g 5.
 ORGANISM Homo sapiens
 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE 1 (bases 1 to 3901)
 AUTHORS Kiefer, M. C., Baird, A., George-Nascimento, C., Nguyen, T., Mason, O. B.,
 Boley, L. J., Valenzuela, P. and Barr, P. J.
 TITLE Molecular cloning of a three-immunoglobulin-like-domain form of a
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 biologically active extracellular domain in a baculovirus system
 JOURNAL Unpublished (1991)
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 BASE COUNT 839 a 1187 c 1139 g 736 t
 ORIGIN

Initial Score = 146 Optimized Score = 878 Significance = 0.00
Residue Identity = 47% Matches = 1050 Mismatches = 912
Gaps = 226 Conservative Substitutions = 0

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	GCG A G G C G C G C G C T G C T T G A A A G C C G C G G A A C C C A A G --- G A C T T T C T C C G G T - C C G A G C T C G G G G G C G C C					
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Gaps = 211 Conservative Substitutions = 0

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1250 X 1260 1270 1280 1290 1300 1310

60	70	80	90	100	110	120
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||| : ||| : | : ||| : | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

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1460 1470 1480 1490 1500 1510

270	280	290	300	310	320	330
-----	-----	-----	-----	-----	-----	-----

GCGTGAGCCTCGTGTGGACGGCTGCCGCTGCCGCCAAGCAGCTG-GGCGAGCTGTGCACC

||| : ||| : | : ||| : | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

GAAAAAGAAAAGCCCCATCCGCAGCTGCTTCCAACCGGCCCCCTGCAGTC--CTGACCCCTAGCTCGTCACC

1520 1530 1540 1550 1560 1570 1580

340	350	360	370	380	390	400
-----	-----	-----	-----	-----	-----	-----

GAG-CGCGACCCCTGCGACCCGACAAGGGCCTCTT--CTGTGA--CTTCGGCTCCCCGGCCAACCGCAAGA

||| : ||| : | : ||| : | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

TTGACATGTACAGTGATA-TAGCTAGCTGTTCTGATCCCTGTGACCCCTACGCGCTGACC--TCTACAACTTTG

1590 1600 1610 1620 1630 1640 1650

410	420	430	440	450	460	470
-----	-----	-----	-----	-----	-----	-----

TGGCGTGTGC-ACCGCCAAAGATGGTGCTCCCTGCATCTCGGTGGTACGGTGTACCGCAGCGGAGAGTCC

||| : ||| : | : ||| : | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

TCTTCCTCTCGCAGCCAAAGATGGTGACCCCTGTGCTTCGGTGGTGGTACCGCAGCGGAGAGTCC

1660 1670 1680 1690 1700 1710 1720 1730

HTTGTAATATATGTGGGATATAATATATATATATATATATATATACAGTTATCTA-AGTTAAATTAAAGTCATT
 1770 1780 1790 1800 1810 . 1820 1830
 1840 1850 1860 1870 1880 1890 1900
 TAAAGTTGTTT---GTGCCTTTTATTTTGTTTTAATGCTTGATATTCAATGTTAGCCTCAATTCTG
 | :
 TGTTTTGTTTAAGTGCTTTGGGATTTAAACTGATAGC-CTCAAACCTCCAA--ACACCAT--AGGTAGG
 1840 1850 1860 1870 1880 1890 1900
 1910 1920 1930 1940 1950 1960 1970
 A-AC--ACCATAGGTAGAACATGTAAGCTTGTCTGATCGTTCAAAGCATGAAATGGATACTTATATGGAAATT
 | :
 ACACGAAGCTTATCTGTGATTCAAAACAAAGGAGACTGCAGTG---GGAATTGTGACCT-GAGTGACTCT
 1910 1920 1930 1940 1950 1960 1970
 1980 1990 2000 2010 2020 2030
 CTGCTCAG---ATAGAATGACAGTCC--GTCAAAACAGAT-TGT-TTGCAAAGGGGGAGGCATC-AGT-GTCT
 | :
 CTG-TCAGAACAAACAAATGCTGTGCAGGTGATAA-AGCTATGTATTGGAA-GTCAGATTCTAGTAGGAA
 1980 1990 2000 2010 2020 2030 2040
 2040 2050 2060 2070 X
 TGGCAGGCTGAT--TTCTAGGT-AGGAAATGTGGTAGCTCACG
 | :
 ATGTGGTCAAATCCCTGTTGGTGAACAAATGGCCTTATTAAGAAATGGCTGG
 2050 2060 2070 2080 X 2090

2. US-07-752-427-1 (1-2075)

MUSFISP12A Mouse FISP-12 protein (fisp-12) gene, complete cds

LOCUS MUSFISP12A 4128 bp ds-DNA ROD 09-JUL-1991
 DEFINITION Mouse FISP-12 protein (fisp-12) gene, complete cds.
 ACCESSION M70641
 KEYWORDS cysteine-rich protein; growth factor-inducible gene.
 SOURCE Mus musculus (sub_species domesticus) liver/kidney DNA.
 ORGANISM Mus musculus
 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 4128)
 AUTHORS Ryseck,R.-P., MacDonald-Bravo,H., Mattei,M.-G. and Bravo,R.
 TITLE Structure, mapping and expression of fisp-12, a growth factor
 inducible gene encoding a secreted cysteine-rich protein
 JOURNAL Cell Growth Differ. 2, 225-233 (1991)
 STANDARD full staff_entry
 FEATURES Location/Qualifiers
 CDS join(1052..1114,1202..1424,1675..1926,2059..2270,
 2642..2938)
 /product="FISP-12 protein"
 /gene="fisp-12"
 /codon_start=1
 mRNA join(833..1114,1202..1424,1675..1926,2059..2270,
 2642..4006)
 /gene="fisp-12"
 TATA_signal 798..804
 /gene="fisp-12"
 exon 833..1114
 /number=1
 /gene="fisp-12"
 intron 1115..1201
 /number=1
 /gene="fisp-12"
 exon 1202..1424
 /number=2
 /gene="fisp-12"
 intron 1425..1674

GGCGAAGCTGACGGCTGGCTGCACCAAGCATGAGACATACCGAGCTAAATTCTGTGGAGTATGTACCGAC

210 220 230 240 250 260 270 280

280 290 300 310 320 330 340 350
GTGCTGGACGGCTGGCTGCCGCTGCGCCAAGCAGCTGGCGAGCTGTGCACCGAGCGCGACCC
GTGCTGGACGGCTGGCTGCCGCTGCGCCAAGCAGCTGGCGAGACTGTGTACGGAGCGTGA
290 300 310 320 330 340 350

350 S 360 370 S 380 390 400 S 410 S 420
TCGACCCCGCACAGGGCCTTTCTGTGACTTCGGCTCCCCGGCCAACCGCAAGATCGCGTGTCACCGCC
TGCGACCCAGAAGGGCTTTCTGTGACTTCGGCTCCCCGGCCAACCGCAAGATCGCGTGTCACCGCC
360 370 380 390 400 410 420

430 440 450 460 470 480 490
AAAGATGGTGCTCCCTGCATTTGGTGGTACGGTGTACCGCAGCGGAGAGTCCTTCCAGAGCAGCTGCAAG
AAAGATGGTGCAACCTGTGTCTTCGGTGGTGGTACCGCAGCGGAGTCCTTCCAAAGCAGCTGCAAA
430 440 450 460 470 480 490

500 510 520 530 540 550 560
TACCAATGCACTTGCCCTGGATGGGGCCGTGGCTGCCCTATGCAGCATGGACGTGCGCCTGCCAGC
TACCAATGCACTTGCCCTGGATGGGGCCGTGGCTGCCCTATGCAGCATGGACGTGCGCCTGCCAGC
500 510 520 530 540 550 560

570 580 590 600 610 620 630
CCTGACTGCCCTTCCCAGGGAGGGTCAAGCTGCCGGAAATGCTGCGAGGAGTGGGTGTGACGGAGCCC
CCTGACTGCCCTTCCCAGGGAGGGTCAAGCTGCCGGAAATGCTGCGAGGAGTGGGTGTGACGGAGCCC
570 580 590 600 610 620 630 640

640 650 660 670 680 690 700
AAGGACCAAACCGTGGTGGCCTGCCCTCGCGCTTACCGACTGGAAAGACACGTTGGCCAGACCCAACT
AAGGACCGCACAGCAGTTGGCCCTGCCCTAGCTGCCCTACCGACTGGAAAGACACATTGGCCAGACCCAACT
650 660 670 680 690 700 710

710 720 730 740 750 760 770 780
ATGATTAGAGCCAACTGCCTGGTCCAGACCACAGAGTGGAGCGCCTGTTCCAAGACCTGTGGATGGCATT
ATGATGCGAGCCAACTGCCTGGTCCAGACCACAGAGTGGAGCGCCTGTTCTAACGACCTGTGGAAATGGGCA
720 730 740 750 760 770 780

790 800 810 820 830 840 850
TCCACCCGGTTACCAATGACAACGCCCTCTGCAGGCTAGAGAAGCAGAGCCGCTGTGCATGGTCAGGCCT
TCCACCCGAGTTACCAATGACAATACCTCTGCAGACTGGAGAAGCAGAGCCGCTGTGCATGGTCAGGCCT
790 800 810 820 830 840 850

860 870 880 890 900 910 920
TGCAGCTGACCTGGAGGGAAACATTAAGAAGGGCAAAAGTGCATCCGTACTCCAAAATCTCCAAGCCT
TGCAGCTGACCTGGAGGGAAACATTAAGAAGGGCAAAAGTGCATCCGGACACCTAAAATCGCCAAGCCT
860 870 880 890 900 910 920

930 940 950 960 970 980 990
ATCAAGTTGAGCTTCTGGCTGCACCAAGCATGAGACATACCGAGCTAAATTCTGTGGAGTATGTACCGAC
GTCAAGTTGAGCTTCTGGCTGCACCAAGCATACAGGGCTAACGTTCTGCAGGGTGTGCACAGAC
930 940 950 960 970 980 990 1000

1000 1010 1020 1030 1040 1050 1060
GGCCGATGCTGCACCCCCCACAGAACCAACCAACCTGCCGGTGGAGTTCAAGTGCCTGACGGCGAGGTGATG
1000 1010 1020 1030 1040 1050 1060

9.	AVINIFUSV	A. Villelandii nitrogen fixatio	3861	145	858	0.00	0
10.	HUMHLAA1	Human HLA-A1 gene	3840	140	855	0.00	0
11.	HSSGPGBH	Pseudorabies virus glycoprote	324	134	853	0.00	0
12.	HSSPVGH	Pseudorabies virus glycoprote	3422	135	852	0.00	0
13.	HS5HCMVCG	Human Cytomegalovirus Strain	229354	158	852	0.00	0
14.	MUSCYR61A	Mouse Cyr61 mRNA, complete cd	2018	408	848	0.00	0
15.	HSSRICP18	Pseudorabies virus ICP18.5 ge	2524	168	846	0.00	0
16.	MUSIL5G	Murine eosinophil differentia	6727	130	844	0.00	0
17.	HUMMHEA	Human MHC class I lymphocyte	4938	129	842	0.00	0
18.	HSEIEP	Equine herpesvirus type 1 imm	8174	131	840	0.00	0
19.	AVHNIFREG	Azotobacter chroococcum nifU,	7099	134	838	0.00	0
20.	SERERYA	S. erythraea eryA gene for 6-	9769	126	838	0.00	0

1. US-07-752-427-1 (1-2075)

MUSFISP12B Mouse FISP-12 protein (fisp-12) mRNA, complete cds

Ordered
3/30

LOCUS MUSFISP12B 2267 bp ss-mRNA ROD 09-JUL-1991
 DEFINITION Mouse FISP-12 protein (fisp-12) mRNA, complete cds.
 ACCESSION M70642
 KEYWORDS cysteine-rich protein; growth factor-inducible gene.
 SOURCE Mus musculus (sub_species domesticus) liver/kidney cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 2267)
 AUTHORS Ryseck,R.-P., MacDonald-Bravo,H., Mattei,M.-G. and Bravo,R.
 TITLE Structure, mapping and expression of fisp-12, a growth factor
 inducible gene encoding a secreted cysteine-rich protein
 JOURNAL Cell Growth Differ. 2, 225-233 (1991)
 STANDARD full staff_entry
 FEATURES Location/Qualifiers
 CDS 138..1184
 /product="FISP-12 protein"
 /gene="fisp-12"
 /codon_start=1
 polyA_signal 2224..2230
 /gene="fisp-12"
 BASE COUNT 570 a 569 c 582 g 546 t
 ORIGIN chromosome 10

Initial Score = 1139 Optimized Score = 1522 Significance = 0.00
 Residue Identity = 74% Matches = 1592 Mismatches = 436
 Gaps = 100 Conservative Substitutions = 0

X	10	20	30	40	50	60
CCCGGGCCGACAGCCCCGAGACG--ACAGCCCAGCGCGTCCCGGGTCCCCACCTCCGACCACCGCCAGCGC						
GAATTCCGCCGACAACCCC-AGACGCCACCGCCTGGAGCGTCCAGACACCAACCTCCG-CCCTGTCCG-AA						
X	10	20	30	40	50	60
70	80	90	100	110	120	130
TCCAGGGCCCCGCGCTCCCCGCTCGCCGCCACCGCGCCCTCC---GC-TCCGC---CCGAGTGCCAACCATG						
TCCAGGGCTCCAGGCCGCCCTCTCGTCGCCTCTGCACCCCTGCTGTGCATCCTCCTACCGC-GTCCCGATCATG						
70	80	90	100	110	120	130
140	150	160	170	180	190	200
ACCGCCGCCAGTATGGGCCCCGTCCGCGTCGCCTCGTGGTCCTCCTCGCCCTCTGCAGGCCGGCGCGTC						
CTCGCCTCCGTCGCAGGTCCCATCAGCCTCGCCT---TGGTGCTCCTCGCCCTCTGCACCCGGCTGAGTACG						
150	160	170	180	190	200	

210 220 230 240 S P 250 260 S 270 S
 GGCCAGAACTGCAAGCGGGCGGTGCCGGTGCCGGAGAGGCCGGCGCGCTGCCCGGGCGTGAAGCCTC
 ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

8. HSSRILCP18	Pseudorabies virus ICP18.5 ge	2524	168	848	7.70	0
9. HUMCANPRA	Human calcium-dependent prote	1154	164	390	7.46	0
10. TTHCAAA	T. thermophilus cytochrome caa	1235	164	286	7.46	0
11. XELRGEE83	x. laevis rrna external transc	865	162	210	7.34	0
12. XELRGGMN3	x. laevis 28s rrna non-transcr	1151	162	243	7.34	0
13. HSSHCMVCG	Human Cytomegalovirus Strain	229354	158	852	7.10	0
	**** 6 standard deviations above mean ****					
14. HUMRETS	Human mRNA for ret proto-onco	989	154	431	6.86	0
15. SERERYFGH	S. erythraea 6-deoxyerythromol	2243	152	394	6.74	0
16. MUSHTF9	Mouse DNA for GC rich region	3725	151	869	6.69	0
17. HVBLE	Barley (<i>H. vulgare</i>) lectin mRN	972	150	405	6.63	0
18. BLYLEC	Barley root-specific lectin m	972	150	405	6.63	0
19. WHTAGGTA	Wheat (<i>T. aestivum</i>) germ agglu	998	149	417	6.57	0
20. HUMVIM	Human vimentin gene, complete	1749	148	717	6.51	0

Query sequence being compared: US-07-752-427-1 (1-2075)

Number of sequences optimized: 69

Results of the optimized comparison of US-07-752-427-1 (1-2075) with:

Data bank : GenBank 69, all entries

Data bank : UEMBL 28_69, all entries

PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	1.00	Window size	11
Gap size penalty	0.33		
Cutoff score	124		
Randomization group	0		
Initial scores to save	20	Alignments to save	10
Optimized scores to save	20	Display context	10

SEARCH STATISTICS

Scores:	Mean 820	Median 821	Standard Deviation 0.00
Times:	CPU 00:00:09.98	Total Elapsed 00:00:16.00	

Number of residues: 458541

Number of sequences optimized: 69

The scores below are sorted by optimized score.

Significance is calculated based on optimized score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init.	Opt.	Sig.	Frame
			Score	Score		
1. MUSFISP12B	Mouse FISP-12 protein (fisp-1	2267	1139	1522	0.00	0
2. MUSFISP12A	Mouse FISP-12 protein (fisp-1	4128	498	954	0.00	0
3. HUMFGFAA	Human fibroblast growth facto	3901	146	878	0.00	0
4. HUMERP	Human erythropoietin gene, co	3398	128	877	0.00	0
5. MUSHTF9	Mouse DNA for GC rich region	3725	151	869	0.00	0
6. HUMSRF	Human serum response factor (4200	134	868	0.00	0
7. MUSERPA	Mouse erythropoietin gene, co	3891	139	867	0.00	0
8. CHKCEF	Chicken CEF-10 protein mRNA,	1805	326	865	0.00	0

10
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 -
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 -
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 -
 -
 -
 0-----*
 SCORE O: 1127 253 380 506 633 759 886 1012 1139
 STDEV -1 9

PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	1.00	Window size	11
Gap size penalty	0.33		
Cutoff score	124		
Randomization group	0		
Initial scores to save	20	Alignments to save	10
Optimized scores to save	20	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	39	38	16.75
Times:	CPU		Total Elapsed
	01:04:13.07		01:15:09.00

Number of residues: 74447152
 Number of sequences searched: 57272
 Number of scores above cutoff: 69

The scores below are sorted by initial score.
 Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Init.	Opt.	Length	Score	Score	Sig.	Frame
**** 65 standard deviations above mean ****								
1. MUSFISP12B	Mouse FISP-12 protein (fisp-1	2267	1139	1522	65.66		0	
**** 27 standard deviations above mean ****								
2. MUSFISP12A	Mouse FISP-12 protein (fisp-1	4128	498	954	27.40		0	
**** 22 standard deviations above mean ****								
3. MUSCYR61A	Mouse Cyr61 mRNA, complete cd	2018	408	848	22.02		0	
**** 17 standard deviations above mean ****								
4. CHKCEF	Chicken CEF-10 protein mRNA,	1805	326	865	17.13		0	
**** 13 standard deviations above mean ****								
5. MMCYR61G	Mouse growth factor inducible	5196	264	833	13.43		0	
**** 8 standard deviations above mean ****								
6. HUMNFILE	Human gene for nuclear factor	1910	181	621	8.48		0	
**** 7 standard deviations above mean ****								
7. PSEPMI	P. aeruginosa pmi gene encoding	1990	170	718	7.82		0	

```
> O<
O: 10 IntelliGenetics
> O<
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-07-752-427-1.res made by maryh on Thu 6 Feb 92 16:25:14-PST.

Query sequence being compared: US-07-752-427-1 (1-2075)
Number of sequences searched: 57272
Number of scores above cutoff: 69

Results of the initial comparison of US-07-752-427-1 (1-2075) with:
Data bank : GenBank 69, all entries
Data bank : UEMBL 28_69, all entries

100000-
-
N -
U50000-
M -
B -
E -**
R -
-
O -
F10000-
- *
S -
E 5000-
Q -
U *
E -
N - *
C -
E -
S 1000-
-
- *
500-
-
-
- *
-
-
-
100-
-
-
50-
- *
-
-
- *
-
-
-

140 150 160 170 180 190
LCSDMDVRLPSPD---CPFPRRVF GKCEEWCDEPKDQTVVGPALAAY -LEDTFGPDPMTMIRA---NC
; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
LGMTDYLVIVEDDDSAIIPCRTTDP----ETPV--TLHNSEGVVVPASYDSRQGFNGTFTVGPYICEATVKKGK
140 150 160 170 180 190

200 210 220 230 240 250 260
LVQT--TEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKISKPIKFE
; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
KFQTIPFNVYALKAT----SELDLEMEALKTVYK-SGETIVVTCAVNNEVVDLQWTYPGEVKKGKITMLE
200 210 220 230 240 250 260

270 280 290 300 310 320 330
LSGCTSMK---TYRAKFCGVCTDGRCCTPHRTTLPV-EFKCPDGEMKKNMMFIKTCACHYNCPGDNDIFE
; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
EIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVKEMKKVTISVHEKGFIIEIKPTFSBLEAVNLHEVKH
270 280 290 300 310 320 330

340 X
SLYYRKMYGDMA
;
FVVEVRAYPPPRIISWLKNNLTL
340 X 350

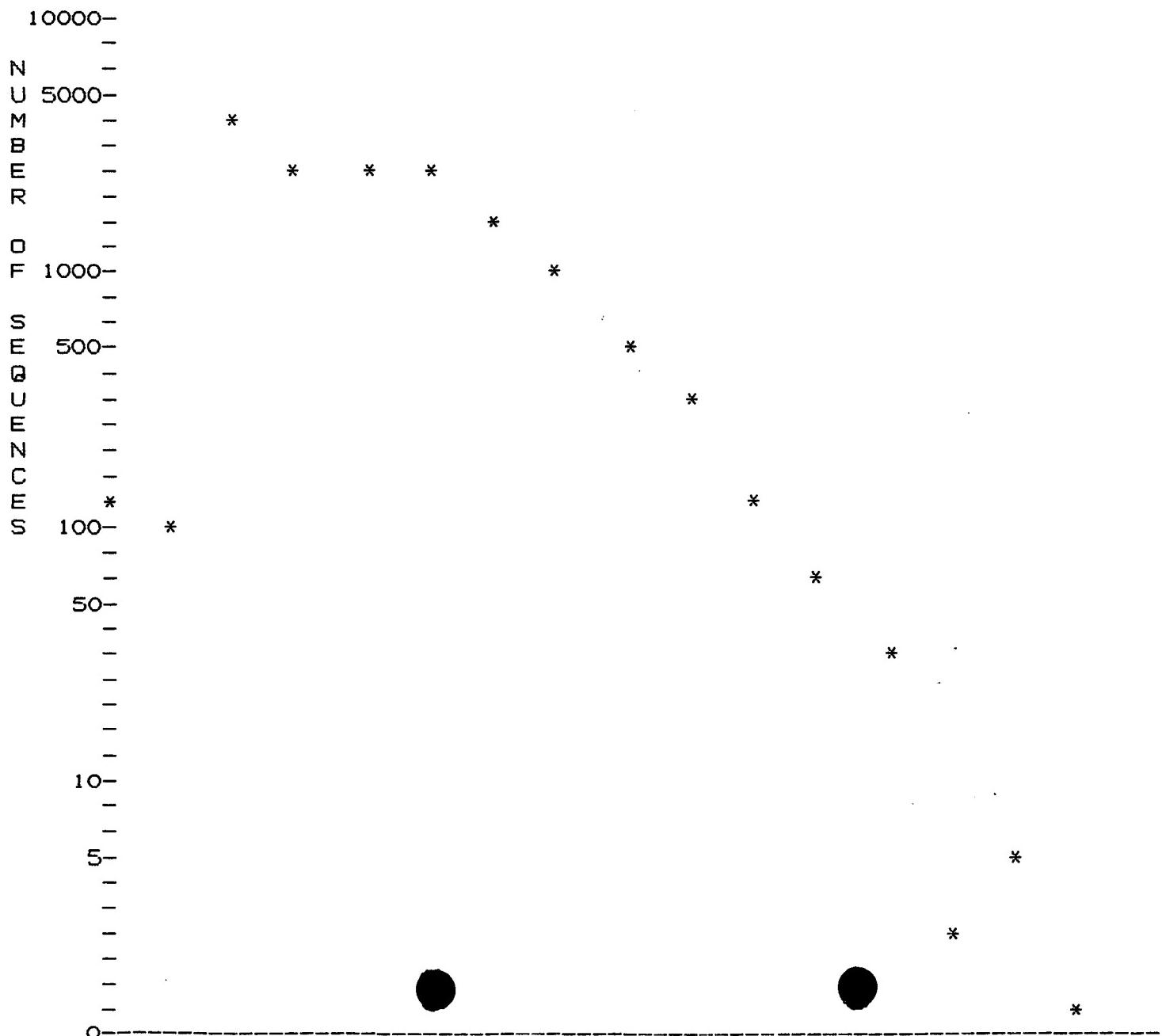
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O: 10 IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-07-752-427-2-a-geneseq.res made by maryh on Thu 6 Feb 92 15:28:31-P

Query sequence being compared: US-07-752-427-2 (1-349)
Number of sequences searched: 14140
Number of scores above cutoff: 3377

Results of the initial comparison of US-07-752-427-2 (1-349) with:
Data bank : A-GeneSeq 5, all entries



SCORE 0: 2 : 3 : 5 : 7 : 8 : 10 : 12 : 13 : 15
 STDEV -1 0 2 3 4 5

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	11
Gap size penalty	0.05		
Cutoff score	6		
Randomization group	0		
Initial scores to save	20	Alignments to save	10
Optimized scores to save	20	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	4	5	2.04

Times:	CPU	Total Elapsed
	00:00:42.09	00:01:27.00

Number of residues:	2168208
Number of sequences searched:	14140
Number of scores above cutoff:	3377

The scores below are sorted by initial score.
 Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

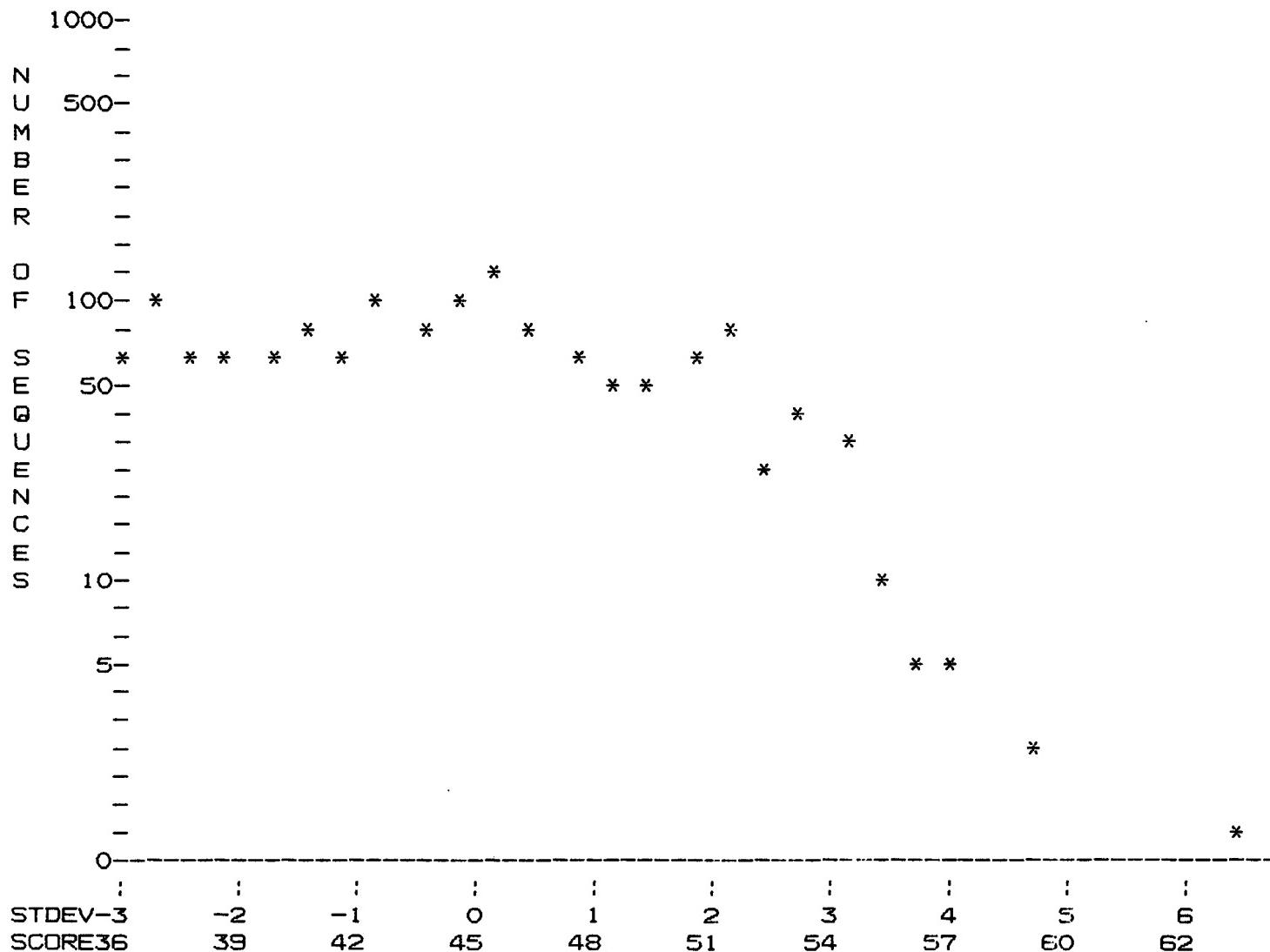
The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
**** 5 standard deviations above mean ****						
1. P93284	Sequence of clone HIV-2 SBL/I	3025	15	57	5.39	0
**** 4 standard deviations above mean ****						
2. P81243	Human spleen trypsin III (try	247	14	37	4.90	0
3. R11741	Granulocyte colony stimulatin	783	14	32	4.90	0
4. R11742	Clone 25-1 encoded human G-CS	801	14	35	4.90	0
5. R08039	Cathepsin D fragment of fibro	993	14	45	4.90	0
6. P70373	Human fibronectin gene produc	2327	14	45	4.90	0
7. R12185	Protease inhibitor with varia	114	13	17	4.41	0
8. P94681	Amino acid sequence encoded b	348	13	25	4.41	0
**** 3 standard deviations above mean ****						
9. R10109	Trigamin-beta 1	72	12	20	3.92	0
10. P91320	New trigamin peptide isolate	72	12	20	3.92	0
11. R10110	Trigamin-beta 2.	73	12	20	3.92	0
12. R10106	Trigamin-gamma.	73	12	19	3.92	0
13. P96395	Albolabrin.	73	12	19	3.92	0
14. R06395	Albolabrin.	73	12	19	3.92	0
15. R07329	Amb a I/Antigen E encoded by	92	12	20	3.92	0
16. R07330	Amb a I/Antigen E encoded by	94	12	21	3.92	0
17. R07455	N-terminal sequence of anti-p	120	12	22	3.92	0
18. P91901	Deduced sequence of porcine e	203	12	34	3.92	0
19. P91376	Porcine endothelin III.	203	12	34	3.92	0
20. P90502	Gp. B Eimeria tenella immunoge	237	12	36	3.92	0

Number of sequences optimized:

3377

Results of the optimized comparison of US-07-752-427-2 (1-349) with:
Data bank : A-GeneSeq 5, all entries



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	11
Gap size penalty	0.05		
Cutoff score	6		
Randomization group	0		
Initial scores to save	20	Alignments to save	10
Optimized scores to save	20	Display context	10

SEARCH STATISTICS

Scores: Mean 45 Median 49 Standard Deviation 3.08

Times: CPU 00:01:28.89 Total Elapsed 00:02:56.00

Number of residues: 1361708
Number of sequences optimized: 3377

The scores below are sorted by optimized score.

Significance is calculated based on optimized score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init.	Opt.	Sig.	Frame
			Score	Score		
**** 5 standard deviations above mean ****						
1. P92069	Human muscarinic acetylcholin	2135	10	63	5.84	0
**** 4 standard deviations above mean ****						
2. P60053	Sequence of von Willebrand fa	2813	11	59	4.54	0
3. P60462	Sequence of human von Willebr	2813	7	59	4.54	0
**** 3 standard deviations above mean ****						
4. P93284	Sequence of clone HIV-2 SBL/I	3025	15	57	3.89	0
5. P80674	NtrA gene product.	523	6	57	3.89	0
6. R10534	Human 160kD mediator of infla	1427	10	57	3.89	0
7. P93357	Sequence of the catalytic dom	1522	9	57	3.89	0
8. R12108	N-terminal deleted adeny1 cyc	1445	9	56	3.57	0
9. R08267	Platelet derived growth facto	1089	6	56	3.57	0
10. R06910	Alpha type PDGF receptor dedu	1089	6	56	3.57	0
11. P94365	Sequence of part of adeny1ate	1705	9	56	3.57	0
12. R07683	gag protein precursor, p75gag	636	6	56	3.57	0
13. P80810	Sequence of pol protein of HI	1014	6	55	3.25	0
14. P90599	Human retinoblastoma.	970	6	55	3.25	0
15. R07713	Human low density lipoprotein	800	8	55	3.25	0
16. P60057	Factor IX/Factor VII fusion p	453	9	55	3.25	0
17. P90180	Tissue plasminogen activator	534	6	55	3.25	0
18. P60056	Factor VII peptide encoded by	466	9	55	3.25	0
19. R08031	Adenyl cyclase from Bordetell	1706	9	55	3.25	0
20. P60055	Partial Factor VII peptide.	371	9	55	3.25	0

1. US-07-752-427-2 (1-349)

P92069 Human muscarinic acetylcholine m2 receptor gene.

ID P92069 standard; protein; 2135 BP.
AC P92069;
DT 27-SEP-1989 (first entry)
DE Human muscarinic acetylcholine m2 receptor gene.
KW Muscarinic acetylcholine receptor; drug screening; probes; m2; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 120..1517
FT /*tag= a
FT /product=MAR subtype m2
FT misc_signal 74
FT /*tag= b
FT /label=splice acceptor site
FT /note=defines the 5' end of the exon
FT polyA_site 74..2096
FT /*tag= c
PN US7241971-A.
PD 14-MAR-1989.
PF 08-SEP-1988; 241971.
PR 08-SEP-1988; US-241971.
PA (USSH) Nat Inst of Health.
DR WPI; 89-165452/22.
DR P-PSDB; P96203.
PT Cloned genes for muscarinic acetylcholine receptors -
PT for drug screening and diagnostic use.
PS Disclosure; p; English.
CC The sequence may be useful for synthesis of hybridisation probes for
CC diagnostic use. The genes are cloned by screening a rat cerebral cortex

CC cDNA library with a probe based on nucleotides 170-223 of the non-coding
CC strand of porcine brain (m1) cDNA (modified at positions 5, 38 and 53);
CC identifying cDNA clones by hybridisation with BamHI or XbaI digests of
CC plasmid DNA from 12 cultures contg. up to 500000 independent clones;
CC reculturing until a pool contg. less than 5000 indep. clones with a
CC single hybridisation band are identified, and isolating individual clones
CC by colony hybridisation.
CC Stable cell lines are produced by transfecting Chinese hamster ovary cells
CC (CHO-K1) with various pCD vectors contg. the gene inserts.
CC See also N92068-N92067 and N90086.

SQ Sequence 2135 BP; 629 A; 462 C; 448 G; 596 T;

Initial Score = 10 Optimized Score = 63 Significance = 5.84
Residue Identity = 20% Matches = 75 Mismatches = 266
Gaps = 20 Conservative Substitutions = 0

X	10	20	30	40	50	60	
MTAASMGPVRAFVVLLALCSRPAVGQNCSGPCRCPDEPAPRCPAGVSLVLDGCGCCRVCAK							
:	:	:	:	:	:	:	
AAAGTCAACCGGCCACCTCCAGACCGTCAACAATTACTTTTATTCAAGCTTGGCCTG-TGCTGACCTTATCAT							
270	X	280	290	300	310	320	330
70	80	90	100	110	120	130	
QLGELECTERDPDCPHKGFLFCDFGSPANRKIGVCT--AKDGAPCIFGGTVYRSGESFQSCKYQCTCLDG--A							
:	:	:	:	:	:	:	
AGGTGTTTCTC-CATGAACTTG-TACACCCTCTACACTGTGATTGGTTACTGGCCTTGGGACCTGTGGTG							
340	350	360	370	380	390	400	
140	150	160	170	180	190	200	
VGCMPLCSMDVRLPSPDCPFPRRVKLPGKCCEEWVCDEPKDQTVVG--PALAAYRLEDTFGPDPPTMIRANCL							
:	:	:	:	:	:	:	
TGTGACCTTGGCTAGCCTGGACTATGTGGTCAGCAATGCCTCAGTTATGAATCTGCTCATCAT--CAGC-							
410	420	430	440	450	460	470	
210	220	230	240	250	260	270	
VQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKG--KKCIRTPKISKPIKFEL							
:	:	:	:	:	:	:	
-TTTGACAGGTACTTCTGT-GTCACAAAAACCTCTGACCTACCCAGTCAAGCGGACCACAAAAATGGCAGGTA							
480	490	500	510	520	530	540	
280	290	300	310	320	330		
SGCTSMKTYRAKFCGVCT-DGRCCCTPHRTTLVFKCPDGEVMKKNMFIKTC---ACHYNCPGDNDIFES							
:	:	:	:	:	:	:	
TGATGATTGCAGCTGCCTGGTCCTCTCTTCTGACCTCTGGCCTCCAGCCATTCTCTGGCAGTTCATG							
550	560	570	580	590	600	610	
340	X						
LYYRKMYGDMA							
:	:						
TAGGGGTGAGAACTGTGGAGG							
620	X	630					

2. US-07-752-427-2 (1-349)

P60053 Sequence of von Willebrand factor (vWF).

ID P60053 standard; Protein; 2813 AA.
AC P60053;
DT 22-JUL-1991 (first entry)
DE Sequence of von Willebrand factor (vWF).
KW Vascular injury; platelet plug formation.
OS Homo sapiens.
PN EP-197592-A.
PD 15-OCT-1986.
PF 26-MAR-1986; 200518.
PR 01-APR-1985; NL-000961.

PR (VRIE-) STICHT VRIEND LANDS.
 PA (FRIN-) STICHT FRINDER RANT.
 PI Pannekoek H, Verwey O, Diergaarde PJ, Hart MHL;
 DR WPI; 86-273504/42.
 DR N-PSDB; N60061.
 PT Recombinant cDNA plasmid or phage - contg. C-DNA fragment which
 PT codes for biological activity of human von Willebrand factor
 PS Disclosure; Fig 3; 37pp; English.
 CC vWF (glyco) protein having the AA sequence corresponding to the
 CC nucleotide sequence of 2518-8667 or 295-2517 of N60061 is claimed.
 CC Also claimed are new microorganisms, animal cell or human cell contg.
 CC the recombinant cDNA plasmid or phage; e.g. strain E. coli DH1 contg.
 CC the recombinant cDNA plasmid pSP8800vWF is deposited as C. B. S. No
 CC 163. 86.
 SQ Sequence 2813 AA:
 SQ 160A; 137R; 101N; 160D; 0 B; 217C; 142Q; 181E; 0 Z; 207G; 77 H;
 SQ 97 I; 233L; 104K; 55 M; 93 F; 173P; 201S; 146T; 27 W; 81 Y; 221V;

 Initial Score = 11 Optimized Score = 59 Significance = 4.54
 Residue Identity = 20% Matches = 77 Mismatches = 248
 Gaps = 43 Conservative Substitutions = 0

X	10	20	30	40	50		
MTAASMGPVRV-AFVVLALCSRPAVGQ-NCSGPC-RCPDEPAPRCPAGVSLVLDGCGCCRV							
:	::	::	::	::	::		
NYNGNQGDDFLTPSGLAEPRVEDFGNAWKLHGDCQDLQKQHSDPCALNPRMTRFSEEACAVLTSPTFEACHR							
530	X 540	550	560	570	580	590	
60	70	80	90	100	110	120	130
CAKQLGELCTER-DPCDPHKGLFCDFGSPANRKIGVCTAKDGAPCIFGGTVYRSGESFQSSCKYQCTCLDGA							
:	::	::	::	::	::		
AVSPLPYLRNCRYDVCSCSDGRECLCGALA-----SYAAACAGRGRVVAWREPGRCELNCPKGQ-VYLQCG							
600	610	620	630	640	650	660	
140		150	160	170	180	190	
VGCMPLCSMDVRLPSPD-----CPFPRRVKLPGKCCEEWVCDEPKDQTVVGPALAAYRLEDTFGPDP							
:	::	::	::	::	::		
TPCNLTC---RSLSYPDEECNEACLEGCFCP----PGLYMDERGDCVPKAQCPYDGEIFQPEDIFSDHH							
670	680	690	700	710	720		
200	210	220	230	240	250	260	
TMIRANCLVQTTEWSACSKTCGMGIISTRVTNDNASCRLEKQS---RLCMV-RPCEADLEENIKKGKKCIRTP							
:	::	::	::	::	::		
TM---CYCEDGFMHCTMSGVPGSLLPDAVLSSPLSHR-SKRSLSCRPPMVKLVCPAD--NLRAEGLECTKT-							
730	740	750	760	770	780	790	
270	280	290	300	310	320	330	
KISKPIKFELSGCTS MKTYRAKFCGVCTDGRCCCTPHRTTLPVEFKCPDGEVMKKNMFIKTCACHYNC-PG							
:	::	::	::	::	::		
CQNYDLECMSMGCVS--GCLCPPGMVRHENRCVALERCPCFHQGKEYAPGETVKIGCNTVCRDRKWNC TDH							
800	810	820	830	840	850	860	
340	X						
DNDIFESLYRKMYGDMA							
:	::	::	::	::	::		
VCDATCSTIGMAHYLTDFGLKYLFPGE C							
870	880						

3. US-07-752-427-2 (1-349)

P60462 Sequence of human von Willebrand Factor (VWF) prec

ID P60462 standard; Protein; 2813 AA.

AC P60462;

DT 25-JUN-1991 (first entry)

DE Sequence of human von Willebrand Factor (VWF) precursor.

KW Chronic renal failure; therapy; factor VIII C.

OS Homo sapiens.

PN W08606096-A.

PD 23-OCT-1986.

PF 10-APR-1986; U00760.

PR 11-APR-1985; US-722108.

PA (CHIL-) CHILDRENS MED CENT.

PA (GINS/) GINSBURG D.

PI Ginsburg D, Orkin SH, Kaufman RJ;

DR WPI; 86-291663/44.

DR N-PSDB; N60404.

PT Pure Von Willebrand Factor - produced using an expression vector

PT including a DNA sequence encoding functional VWF protein

PS Disclosure; Table 2, Pages 18-36A; 54pp; English.

CC cDNA clones pVWH33, pVWH5 and PVWE6 which span 9 kb pairs of DNA and
CC encompass the entire protein coding region of VWF, were selected to
CC construct full length cDNA (N60404). The pure VWF produced is useful
CC in the treatment of von Willebrand's disease (VWD) and the patients
CC with chronic renal failure whose abnormal bleeding times are
CC corrected by crude cryoprecipitate. Pure VWF can also be used to
CC carry, stabilise and improve the therapeutic efficacy of factor
CC VIII:C.

SQ Sequence 2813 AA;

SQ 154A; 143R; 98 N; 155D; 0 B; 234C; 133Q; 181E; 0 Z; 205G; 70 H;

SQ 95 I; 227L; 108K; 56 M; 89 F; 176P; 207S; 151T; 26 W; 79 Y; 226V;

Initial Score = 7 Optimized Score = 59 Significance = 4.54
Residue Identity = 20% Matches = 76 Mismatches = 259
Gaps = 28 Conservative Substitutions = 0

X 10 20 30 40 50 60
MTAASMG-PVRVAFVVLLALCSRPAV-GIACNSGPCRCPCDEPAPRCPAGVSLVLDGCGCCRC

: :

CLPDKVCVHRSTIYPVGQFWEEGCDVCTCTDMEDAVMGLRVAQCSQKPCE--DSCRSGFTYVLHEGECCGRC
2430 X 2440 2450 2460 2470 2480 2490

70 80 90 100 110 120

AKQLGELCT---ERDPCDPHKGLFCDFGSPAN-RKIGVCTAKDGAPCIFGGTV-YRSGESFQSSCKYQCTCL
: :

LPSACEVVTGSPRGDSQSSWKSVGSQWASPENPCLI NECVRVKEEVFIQQRNVSCPQLEVPVCPSGFQLSCK
2500 2510 2520 2530 2540 2550 2560

130 140 150 160 170 180 190
DGAVGCMPLCSMDVRLPSPDCPFP RRVKLPKGKCCEEWVCDEPKDQTVVGPALAA YRLE---DTFGPDPTMIR
: :

TSA--CCPSC---RCERMEACMLNGTVIGPGKTV MIDVCTTCRCMVQVG-VISGFKLECRKTTCNPCP--LG
2570 2580 2590 2600 2610 2620 2630

200 210 220 230 240 250 260
ANCLVQTTEWSACS KTCGMGI STRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKISKPIKF
: : : : : : : : : : : : : : : : : : : :

YKEENNTGECCGRCLPTACTIQLRGQIMTLKRDET LQDGCDTHFC-KVNERGEYFWEKRV TGCPPFDEHKC
2640 2650 2660 2670 2680 2690 2700

270 280 290 300 310 320 330
ELSGCTS MKTYRAKFCGVCTDGR CCTPHRTTTL-PVEFKCPDGEVMKKNM MF IKTCACHYNCPGD-ND--IF
: : : : : : : : : : : : : : : : : : : :

LAEGGKIMK-IPGTCCDTCEEPEC--NDITARLQYVKVG SCKSEVEVDIHYCQGK CASKAMYSIDINDV QDQ
2710 2720 2730 2740 2750 2760 2770

340 X

ESLYYRKMYGDMA

: : :

CSCCS PTRTEPMQVALHCTNGS

2780 X 2790

4. US-07-752-427-2 (1-349)

P93284 Sequence of clone HIV-2 SBL/ISY.

ID P93284 standard; protein; 3025 AA.
AC P93284;
DT 06-APR-1990 (first entry)
DE Sequence of clone HIV-2 SBL/ISY.
KW HIV-2; proviral clone HIV-2 SBL/ISY;
OS Human immunodeficiency virus 2.
PN US7331212-A.
PD 29-AUG-1989.
PF 31-MAR-1989; 331212.
PR 31-MAR-1989; US-331212.
PA (USSH) US Dept. Health and Human Services.
PI Franchini G, Wong-Staal F, Gallo R;
DR WPI; 89-339698/46.
DR N-PSDB; N92119.
PT Complete human immunodeficiency type 2 proviral clone - used to generate animal model for function studies of HIV genes in vivo.
PS Disclosure; Fig. 5; 43pp; English.
CC The protein is encoded by the second reading frame of HIV-2 SBL/ISY, a proviral clone of HIV-2.
SQ Sequence 3025 AA;
SQ 143 A; 278 R; 126 N; 104 D; 0 B; 96 C; 191 Q; 115 E; 0 Z; 244 G;
SQ 95 H; 153 I; 224 L; 246 K; 65 M; 63 F; 160 P; 291 S; 193 T; 53 W;
SQ 80 Y; 105 V;

Initial Score = 15 Optimized Score = 57 Significance = 3.89
Residue Identity = 20% Matches = 75 Mismatches = 256
Gaps = 41 Conservative Substitutions = 0

	10	20	30	40	50	
X						
MTAASMGPVRAFVVLLALCSRPAVGQNCSPGCRCPDDEPA						PRCPAGVSLVLDGC
:	:	:	:	:	:	:
MDSHPETSGCPKLGGTNLPRNKDQTLMA						
980	990	1000	1010	1020	1030	1040
CRVCAK---QLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAKDGAPCIFGGTVYRSGESFQSSCKYBCT						
RSNSSKGSRQSVDISTPGRKNSKSRKICKDKKKPYQRGQVVGT						
1050	1060	1070	1080	1090	1100	1110
CLDGAVGCMPLCS-MDVRLPSPDCPFPRRVKLPGKCCEEWVCDEPKDQTVVGPALAA						
DLGTVVG--LLASDMMDPRLGLRIHPTVGQVSIPGKRSYTRRRD						
1120	1130	1140	1150	1160	1170	1180
PTMIRANLVATTEWSACSKTCGMGISTRVTNDNASCRL						
SKDIRAN--YQPT--SRIRSLCNGSNRLRSKSQYCS-RLTVCNGNSRPTGIRENSKNYRRDDKKGSNLCCM						
1190	1200	1210	1220	1230	1240	
TP-KISKPIKFELSGCTS-MKTYRAKFCGVCTDGR-CCTPHRTTLPVEFKCPDGEVMKKNMFIKTCACHY						
GPGPQRHRRKSRNPLSKSGHQTSIIPRENRARSGRTWKISQCKRTSPVWITQPGGKTN SKHMCVPVPTKRGSY						
1250	1260	1270	1280	1290	1300	1310
330	340	X				
NCPGDNDIFESLYYRKMYGDMA						
:	:					
-TWASKCRTRHLANGLHTLRMKNHYSSTCCK						

10. *Urtica dioica* L. (Nettle) (Figure 10)

5. US-07-752-427-2 (1-349)

P80674 NtrA gene product.

ID P80674 standard; protein; 523 AA.
AC P80674;
DT 24-OCT-1990 (first entry)
DE NtrA gene product.
KW NtrA; sigma factor; transcriptional activation; nitrogen assimilation;
KW fixation; nif operon; C4-dicarboxylate transport.
OS Rhizobium meliloti.
PN EP-292984-A.
PD 30-NOV-1988.
PF 27-MAY-1988; 108482.
PR 29-MAY-1987; US-055228.
PA (GEHO-) Gen Hospital Corp.
PI Ronson C, Ausubel F;
DR WPI; 88-339561/48.
DR N-PSDB; N81266.
PT Cloned rhizobium meliloti ntrA gene - for use in C4-dicarboxylate
PT transport, nitrate assimilation, symbiotic nitrogen fixation and
PT identifying pathogenic genes.
PS Claim 1; Page 12; 19pp; English.
CC The ntrA gene product is a transcriptional activator. It controls the
CC processes of nitrate assimilation, symbiotic nitrogen fixation and
CC C4-dicarboxylate transport, working in conjunction with NtrC, NifA and
CC DCtD resp. It can also be used to identify genes involved in
CC pathogenesis.
CC See also P82126.
SQ Sequence 523 AA;
SQ 60 A; 43 R; 15 N; 43 D; 0 B; 4 C; 25 Q; 39 E; 0 Z; 29 G; 12 H;
SQ 23 I; 58 L; 15 K; 13 M; 17 F; 25 P; 37 S; 21 T; 3 W; 8 Y; 33 V;

Initial Score = 6 Optimized Score = 57 Significance = 3.89
Residue Identity = 20% Matches = 75 Mismatches = 257
Gaps = 39 Conservative Substitutions = 0

	X	10	20	30	40	50	
MTAASMGPVRAVFVLLALCSRPA--VGQNCSPCPCPDEP--APRCPAGVSLVLDGCGCCR	:	:	:	:	:	:	
LHLRQSQSLVMTPQLMOSIQLLQMNHLELSHFIABEVEKNPLLEVQPADEPTISDREDAGPHPAETG-GETD	10	X 20	30	40	50	60	70
VCAKQ--LGELCTERDPDCPHKGGLFCDFGSPANRKIGVCTAKDGAPCIFGGTVYRSGESFQSSCKYQCTCLD	60	70	80	90	100	110	120
EAAGQSDLYDSAMSRSGERLSEGDDADF---AN-VFPDDTAPQRADAPELLGQWKSMMPGAGDAEGY--DLDD	80	90	100	110	120	130	140
GAVGCMPL-CSMDVRLP-----SPDCPFPRRVKLPGKCCEWVCDEFKDQTVVGPA--LAAYRLEDTFGPDP	130	140	150	160	170	180	190
FVGGRKTLRETLAEQLPFALSAVSDRLIARYFIDQQLDAGYLHADLAETAETLGAAGEDVARVLHVLQQFDP	150	160	170	180	190	200	210
TMIRANCLVQTTEWSA---CSKTCGMGIISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTP	200	210	220	230	240	250	260
PGVFARTL---GECLAIQLRARNRLDPAMEALVANLELLARRDFASLKKICGVDEEDLIIDMLAEIRKLDPKP	220	230	240	250	260	270	280
KIS-KPIKFELSGCTS MKTYRAKPCGVCTDGRCCPHRTTLPVEFKCPD--GEVMKKNMMFIKTCACHYNC	270	280	290	300	310	320	

GTSFETGVFE--R11PDUVVRA----APDGGWLVELNPDALPRVLVNHDYFTE1SRSRKNSGEQAFLNEL
 290 300 310 320 330 340
 330 340 X
 -PGDNDIFESLYYRKMYGDMA
 : : :
 LQNANWLTRSLDQRARTIMKVASEIVRQQDA
 350 360 370 380

6. US-07-752-427-2 (1-349)

R10534 Human 160kD mediator of inflammation protein.

ID R10534 standard; Protein; 1427 AA.
 AC R10534;
 DT 12-APR-1991 (first entry)
 DE Human 160kD mediator of inflammation protein.
 KW Mediator of Imflammation; cytokine; Hodgkin's lymphoma; MRP-160.
 OS Homo sapiens.
 PN EP-412050-A.
 PD 06-FEB-1991.
 PF 26-JUN-1990; 810481.
 PR 05-JUL-1989; GB-015414.
 PA (CIBA) CIBA GEIGY AG.
 PI Odink KG, Tarcsay L, Bruggen J, Wiesendanger W, Cerletti N;
 PI Sorg C, Dewolf-Peeters C, Delabie J;
 DR WPI; 91-038913/06.
 DR N-PSDB; Q10378.
 PT 160 kD human polypeptide mediator or precursor of inflammation -
 PT polyclonal or monoclonal antibodies to polypeptide treat and
 PT diagnose chronic inflammation and hodgkins lymphoma
 PS Claim 3; Page 32; 47pp; English.
 CC The protein is a cytokine used to treat chronic inflammatory
 CC conditions. It is prepared by chromatographically purifying an
 CC optionally pre-purified cell extract, cell supernatant or cell
 CC filtrate of stimulated normal human leucocytes or human embryonic
 CC epithelial lung cells. Alternatively, the protein can be produced
 CC by microorganisms or continuous mammalian cell lines, transformed
 CC with plasmids encoding MRP-160. The invention also covers the
 CC polypeptide fragment from amino acids 878-1427 and derivatives of
 CC the protein in which the amino and/or hydroxyl functions are
 CC glycosylated or acylated and have mol. wt.s of 190 and 140kD,
 CC respectively.
 SQ Sequence 1427 AA;
 SQ 115A; 67 R; 59 N; 70 D; 0 B; 14 C; 90 Q; 199E; 0 Z; 49 G; 26 H;
 SQ 45 I; 156L; 153K; 33 M; 29 F; 34 P; 121S; 88 T; 5 W; 9 Y; 65 V;

Initial Score = 10 Optimized Score = 57 Significance = 3.89
 Residue Identity = 19% Matches = 73 Mismatches = 258
 Gaps = 39 Conservative Substitutions = 0

	X	10	20	30	40	50	60
	MTAASMGPVRAFVVLLALCSRPAVGQNCSPCRCPDE--PAPRCPAGVSLVLDGCGCCRVC						
	:	:	:	:	:	:	:
	SNLTKTASESISNLSEAGSIKKGERELKIGDRVLVGGTKAGVVRFLEGETDFAKGEWCGVELDEPLGKNDGAV						
190	X 200	210	220	230	240	250	
	70	80	90	100	110	120	
	AKQLGELC--TERDPCDPHKGLCDFGS--PANRKIGVCTAKDGAFCAFGGTVYRS-GESFQSSCKYQCTCL						
	:	:	:	:	:	:	
	AGTRYFQCQPKYGLFAPVHKVTKIGFPSTTPAKAK---ANAVRRVMATTSASLKRSPSASSLSSMSSVASCV						
260	270	280	290	300	310	320	
	130	140	150	160	170	180	190
	DGAvgcmpl---	CSMDVRLPSPDCPFPRRVKLPGKCCEEWVCDEPKDQTVVGPALAAYRLEDTFGPDPPTMI					
	:	:	:	:	:	:	

SSRPSRIGLLTEISSRYARKISGITALQEALKERQDWHIEQLLAERDLERAEVAKA-15AVGETEDELALARD
330 340 350 360 370 380 390

330 340 350 360 370 380 390

200	210	220	230	240	250	260
RANCLVQTTEWSACSKTCGMGISTRV-TNDNASCRLEKQSRLCMVRPCEADL-----EENIKKGKKCIRTPK						
400	410	420	430	440	450	460
270	280	290	300	310	320	330
ISKPIKFELSGCTS MKTYRAKFCGVCTDGRCCT---PHRTTLPVEFKCPDGEVMKKNM MFIKTCACHYNCP						
470	480	490	500	510	520	
EHARIKELEQSLLFEKTKADKLQRELEDTRVATVSEKS RIM ELEKDLALRVQE V-----AELRRRLESNKP						

340	X	
-GDNDIFESLYYRKMYGDMA		
AGDVDMMSLQLQEISSLQEKELEVTRTDHQ		
530	540	550

7. US-07-752-427-2 (1-349)

P93357 Sequence of the catalytic domain of *Bordetella pertussis*

ID P93357 standard; protein; 1522 AA.
AC P93357;
DT 22-MAR-1991 (first entry)
DE Sequence of the catalytic domain of *Bordetella pertussis*
DE adenylate cyclase (AC).
KW Vaccine; ss.
OS *Bordetella pertussis*.
PN FR2618453-A.
PD 27-JAN-1989.
PF 24-JUL-1987.
PR 24-JUL-1987; FR-010589.
PA (INSP) Inst Pasteur.
PI Danchin A, Glaser P, Ullmann A.
DR WPI; 89-079098/11.
DR N-PSDB; N90659.
PT Cloning and expressing genes in multi-protein function system - by
PT transforming host cell with indicator gene producing protein which
PT interacts with expression prod. of the gene being cloned.
PS Claim 14; Fig 2(a-f); 24pp; French..
CC Sequences encoding at least a part of AC able to hybridise with a
CC gene expressing a protein with AC activity, and proteins with AC
CC activity able to form immune complexes with specific antibodies, are
CC claimed. The isolated AC gene can be used to produce *Bordetella*
CC pertussis toxin.
SQ Sequence 1522 AA;
SQ 206A; 95 R; 55 N; 121D; 0 B; 8 C; 66 Q; 75 E; 0 Z; 190G; 32 H;
SQ 61 I; 123L; 41 K; 24 M; 36 F; 40 P; 93 S; 86 T; 13 W; 36 Y; 121V;

Initial Score = 9 Optimized Score = 57 Significance = 3.8
Residue Identity = 19% Matches = 71 Mismatches = 25
Gaps = 35 Conservative Substitutions =

X 10 20 30 40 50 60
MTAASMGPVRAFVVLLALCSRPAVGQNCNSGPCRCPDEPAPRCPAGVSLVLDGCGCCRVCAK

KRTENVQYRHVELARVGQV-VEVDTLEHVQHIIGGAGNDSITGNAHD----NFLAGGSGDDRLDGGAGNDL
1030 1030 1040 1050 1060 1070 1080

70 80 90 100 110 120 130
QLGELCTERDPDPHKGLFCDFG--SPANRKIGVCTAKDGAPCIFGGTVYRSGESFQSSCKYQCTCLDGAV
||| :| :| :| :| :| :| :| :|

VGGEGGGNTV1GGAGAGUDVFLWDLGVWSLDDGGAGVDTVKYNVH&PSEERLERMG----DTG1HADLWKGTV
 1090 1100 1110 1120 1130 1140 1150
 140 150 160 170 180 190
 GCMP---LCSMDVRLPSPDCPFPR---RVKLPGKCCEEWVCDEPKDQTVVG---PALAAYRLEDT-FGPDPTM
 : : : : : : : : : : : : : : : :
 EPWPALNLFSVDHVKNIENLHGSRLLNDRIAGDDQDNELWGHGDGNDTIRGRGGDDILRGGLGLDTLYGEDGND
 1160 1170 1180 1190 1200 1210 1220
 200 210 220 230 240 250 260
 IRANCLVQTTEWSACSKTCGMGIISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKISKPI
 : : : : : : : : : : : : : : : :
 I----FLQDDETVSDDIDGGAGLHT-VDYSAMIHPGRIVAPHEYGFGIEADLSREWVRKASALGVDYYDNVR
 1230 1240 1250 1260 1270 1280
 270 280 290 300 310 320 330
 KFELSGCTSMK---TYRAKFCGVCTDGRCCPHRTTLPVEFKCPDIGEVMKKNMMFIKTCACHYNCPGDNDI
 : : : : : : : : : : : : : : : :
 NENVIGTSMKDVLIGDAQANTLMGQGGDDTGAAATANDLLF-GGDGNDMLYGDAGNDT---LYGGLGD-DT
 1290 1300 1310 1320 1330 1340 1350
 340 X
 FESLYYRKMYGDMA
 : :
 LEGGAGNDWFGQTQAREHDVLRGG
 1360 1370 1380

8. US-07-752-427-2 (1-349)

R12108 N-terminal deleted adenylyl cyclase from *Bacillus* sp

ID R12108 standard; protein; 1445 AA.
 AC R12108;
 DT 30-JUL-1991 (first entry)
 DE N-terminal deleted adenylyl cyclase from *Bacillus* sp.
 KW cyclic adenosine monophosphate; cAMP; NDPK.
 OS *Bacillus pertussis*.
 PN W09106664-A.
 PD 16-MAY-1991.
 PF 31-OCT-1990; F00793.
 PR 31-OCT-1989; FR-014328.
 PR 12-APR-1990; FR-004754.
 PA (INSP) INST PASTEUR.
 PI Lacombe ML, Veron M, Mock M, Barzu O, Sarfati R;
 DR WPI; 91-164211/22.
 DR N-PSDB; Q11826.
 PT Partly new substd. adenosine di- and tri-phosphate derivs. prodn.
 PT - useful as laboratory reagents e.g. affinity chromatography
 PT ligands or fluorescence markers
 PS Claim 11; Fig 1; 54pp; French.
 CC This protein is an N-terminal deletion of the protein encoded by
 CC *B. pertussis* "cya" gene. The first 261 N-terminal amino acids have
 CC been deleted, without affecting the adenylyl cyclase activity of the
 CC protein. The truncated adenylyl cyclase was obtained by unidirectional
 CC deletion of the full-length cya gene, followed by expression in
 CC protease-deficient *E. coli*. The truncated enzyme is useful for
 CC synthesis of cAMP and adenosine phosphate derivatives; to separate
 CC chemically synthesised 3'-substituted ATP derivatives and as a
 CC reagent for assay of pyrophosphate, cAMP and calmodulin.
 CC See also Q11825 and W09106671-A.
 SQ Sequence 1445 AA;
 SQ 188A; 76 R; 58 N; 142D; 0 B; 0 C; 63 Q; 74 E; 0 Z; 214G; 27 H;
 SQ 58 I; 126L; 31 K; 17 M; 34 F; 31 P; 77 S; 67 T; 13 W; 34 Y; 115V;

Initial Score = 9 Optimized Score = 56 Significance = 3.57
 Residue Identity = 19% Matches = 70 Mismatches = 259

	X	10	20	30	40	50	60
	MTAASMGPVRAVVFVLLALCSRPAVGQNCNSGPCRCPDEPAPRCPAGVSLVLDGCGCCRVCAK						
KRTENVQYRHVELARVGQV-VEVDTLEHVQHIIGGAGNDSITGNAHD----NFLAGGSDDRLDGGAGNDTL							
730 X 740 750 760 770 780							
	70	80	90	100	110	120	130
QLGELCTERDPCDPHKGLFCDFGSPAN---RKIGVCTAKDGAPCIFGGTVYRSGESFQSSCKYQCTCLDGAV							
VGGEGQNTVIGGAGDDVFLQDLGVWSNQLDGGAGVDTVKYNVHQPSSEERLERMG----DTGIHADLQKGTV							
790 800 810 820 830 840 850							
	140	150	160	170	180	190	
GCMP---LCSMDVRLPSPDCPFPR---RVKLPGKCCEEWVCDEPKDQTVVG--PALAAYRLEDT-FGPDPTM							
EKWPALNLFSVDHVKNIENLHGSRLNDRAGDDQDNELWGHGDGNDTIRGRGGDDILRGGLGLDLYGEDGND							
860 870 880 890 900 910 920							
	200	210	220	230	240	250	260
IRANCLVQTTEWSACSKTCGMGIISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKISKPI							
I----FLQDDETVSDDIDGGAGLDT-VDYSAMIHPGRIVAPHEYFGIEADLSREWVRKASALGVVDYYDNVR							
930 940 950 960 970 980 990							
	270	280	290	300	310	320	330
KFELSGCTSMK---TYRAKFCGVCTDGRCCCTPHRTTLPVEFKCPDGEVMKKNMFIKTCACHYNCPGDNDI							
NVENVIGTSMKDVLIGDAQANTLMGQGGDDT-VRGGDGDDLLFGGGDGNDMLYGDAGNDT---LYGGLGD-DT							
1000 1010 1020 1030 1040 1050 1060							
	340	X					
FESLYYRKMYGDMA							
LEGGAGNDWFGQTQAREHDVLRGG							
1070 X 1080							

9. US-07-752-427-2 (1-349)

R08267 Platelet derived growth factor (PDGF) receptor protein

ID R08267 standard; protein; 1089 AA.

AC R08267;

DT 07-MAR-1991 (first entry)

DE Platelet derived growth factor (PDGF) receptor protein.

KW Atherosclerosis; fibrotic diseases.

OS Homo sapiens.

PN W08014425-A.

PD 29-NOV-1990.

PF 21-MAY-1990; U02849.

PR 22-MAY-1989; US-355018.

PA (ZYMO-) ZYMOGENETICS INC.

PI Kelly JD, Murray MJ;

DR WPI; 90-375992/50.

DR N-PSDB; Q06869.

PT DNA encoding platelet-derived growth factor - used to transform cells for culturing to detect PDG agonists and antagonists

PT Claim 1; Fig 1; 30pp; English.

CC Gene product may be expressed from a transformed cell. It has utility in detection of PDGF agonist and antagonist analogues, binding AA, AB and BB isoforms. PDGF agonists may be used to enhance wound healing, and antagonists may be used to block the effects of PDGF eg. in treatment of atherosclerosis or fibrotic diseases.

SQ Sequence 1089 AA;

SQ 54 A; 44 R; 44 N; 66 D; 0 B; 17 C; 25 Q; 94 E; 0 Z; 58 G; 25 H;

Initial Score = 6 Optimized Score = 56 Significance = 3.57
 Residue Identity = 19% Matches = 72 Mismatches = 251
 Gaps = 44 Conservative Substitutions = 0

	X	10	20	30	40	50	60
MTAASMGPVRAVAFVVL-LALCSRPAVGQNCSGPCRCPDEAPRCPAGVSLVLDGCGCCRV							CAKQLGEL
			;	;	;	;	;
MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGES	E	V	S	W	Q	P	M
X	10	20	30	40	50	60	
70	80	90	100	110	120	130	
CTERDPCDPHKGLFCDFGSPANRKIGVCTAKDGAPCIFGGTVY				RSGESFQSSCKYQCTCLDGAVGCMP			
		;	;	;	;	;	;
DVEIRNEENNNSGLF	-----	VTLLEVSSA	--SAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVP				
70	80	90	100	110	120	130	
140	150	160	170	180	190		
LCAMDVRLPSPD	---CPFPRRVKLPGKCCEEWVCDEPKDQTVVGPALAAYR	--LEDTFGPDPPTMIRA	---NC				
	;	;	;	;	;	;	;
LGMTDYLVIVEDDDSAIIPCRTTDP	----ETPV	--TLHNSEGVPASYDSRQGFNGTFTVGPYICEATVKKGK					
140	150	160	170	180	190		
200	210	220	230	240	250	260	
LVQT	--TEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKISKPIKE						
	;	;	;	;	;	;	;
KFQTIPFNVYALKAT	----SELDLEMEALKTVYK-SGETIVVTCAVFNNEVVDLQWTYPGEVKKGKGITILE						
200	210	220	230	240	250	260	
270	280	290	300	310	320	330	
LSGCTSMK	---TYRAKFCGVCTDGRCCTPHRTTLPV-EFKCPDGEVMKKNMFIKTCACHYNCPGDNDIFE						
	;	;	;	;	;	;	;
EIKVPSIKLVYTLPVPEATVKDSGDDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKH							
270	280	290	300	310	320	330	
340	X						
SLYYRKMYGDMA							
;							
FVVEVRAYPPPRISWLKNLTL							
340	X	350					

10. US-07-752-427-2 (1-349)

R06910 Alpha type PDGF receptor deduced from TR4 cDNA clone

ID R06910 standard; protein; 1089 AA.
AC R06910;
DT 16-JAN-1991 (first entry)
DE Alpha type PDGF receptor deduced from TR4 cDNA clone.
KW Platelet derived growth factor; T11.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 1.. 23
FT /label=signal peptide
FT Domain 24.. 524
FT /label=ligand binding domain
FT Domain 525.. 548
FT /label=transmembrane region
FT Domain 549.. 599
FT /label=juxtamembrane domain
FT Binding-site 600.. 627
FT /label=ATP binding site
FT Modified-site 849
FT /label=tyrosine autophosphorylation site
FT Modified-site 42.. 44

FT /label=N-glycos_site
FT Modified-site 76..78
FT /label=N-glycos_site
FT Modified-site 103..105
FT /label=N-glycos_site
FT Modified-site 179..181
FT /label=N-glycos_site
FT Modified-site 353..355
FT /label=N-glycos_site
FT Modified-site 359..361
FT /label=N-glycos_site
FT Modified-site 458..460
FT /label=N-glycos_site
FT Modified-site 468..470
FT /label=N-glycos_site

PN W09010013-A.

PD 07-SEP-1990.

PF 08-FEB-1990; U00617.

PR 09-FEB-1989; US-308282.

PA (USDC) US SEC OF COMMERCE.
PI Matsui T, Aaronson SA, Pierce JH

DR WPI; 90-290306/38.

DR N-PSDB; Q05989.

PT Type alpha platelet-derived growth factor receptor gene - useful
PT for transforming cells to express novel protein receptor and also
PT susceptible to genetic engineering.

PS Claim 7; Fig 3; 64pp; English.

The TR4 clone is the largest cDNA clone related to the T11 genomic clone, isolated from a library prep'd. from human thymus DNA. The T4 cDNA clone was isolated from a M426 human embryo fibroblast cDNA library. The coding region can be introduced into the pSV2 gpt vector with a simian sarcoma virus LTR as a promoter and expressed in a host. The resulting protein is a novel PDGF receptor designated type alpha (the known receptor is designated type beta). The polypeptide has a calculated molecular mass of 120 kD and has all the characteristics of a membrane spanning tyrosine kinase receptor. The extracellular region comprises a hydrophobic signal peptide and a ligand binding domain which has structural homology with the PDGF-R/CSF1-R subfamily. Ten Cys residues are spaced at the same positions as in other receptors of the subfamily and eight potential N-linked glycosylation sites are also present. A hydrophobic segment spans the membrane and the cytoplasmic region comprises a juxtamembrane region, a tyrosine kinase region split into TK1 and TK2 by a hydrophilic interkinase region and a hydrophilic C-terminal tail. The TK region includes the consensus ATP binding sequence (G-X-G-X-X-G...K) and a tyrosine autophosphorylation site homologous to that of pp60(v-src).

SQ Sequence 1089 AA;

SQ 54 A; 44 R; 44 N; 66 D; O B; 17 C; 26 Q; 93 E; O N; 58 G; 25 H

SQ 70 I: 104L: 69 K: 26 M: 32 F: 51 P: 93 S: 68 T: 13 W: 47 Y: 89 V:

Initial Score = 6 Optimized Score = 56 Significance = 3.57
Residue Identity = 19% Matches = 72 Mismatches = 251
Gaps = 44 Conservative Substitutions = 0

\times 10 20 30 40 50 60

MTAASMGPVRAFVVL-LALCSRPAVGQNCGPGCRCPDEPAPRCPAIGVSLVDGCGCCRV-----CAKQLGEI

.....

MGTSHPAFLVLGCLL TGLSL ILCQLSLPSI LPNENEK VVQLNSSFSLRCFG ESEVSWQYR

X 10 20 30 40 50

CTERDPCDPHKGLFCDFGSPANRK IGVCTAKDGAPCIFGGTVY----RSGESFQSSCKYQCTCLDGAVGCMPP

RNEENNSGI E-----VTE EVSSA--SAAHIGI VTCVYNTATEHNEI EGRHIVI YVPR

DE VREEKENSCHIJF, V. V. VEELEN, C. VAN DER HORST, DE VREEKENSCHIJF, J. VAN DER HORST